

**In the Claims:**

Please replace the claims with the following listings of claims:

1. to 5. (Canceled).
6. (Currently Amended) A diagnostic system for quantitating the individual contribution of a mutation or combination of mutations to a drug resistance phenotype exhibited by an HIV strain, said system comprising  
means for obtaining a genetic sequence of said HIV strain;  
means for identifying the mutation pattern in said genetic sequence as compared to wild  
type HIV; and  
means for predicting the fold resistance exhibited by said HIV strain A method for  
quantitating the individual contribution of a mutation or combination of mutations to a  
drug resistance phenotype exhibited by HIV, said using a method comprising the steps of:  
1a) performing a linear regression analysis using data from a dataset of matching genotypes and phenotypes, wherein the log fold resistance, pFR, of each said HIV strain is modeled as the sum of all the individual resistance contributions for each of said mutations or combinations of mutations that occur in HIV according to the following equation;

$$pFR = \beta_A M_A + \beta_B M_B + \beta_n M_n + \dots + \beta_Z M_Z + \varepsilon$$

wherein each said individual resistance contribution is calculated by multiplying a mutation factor,  $M_A, M_B, \dots, M_Z$ , for each of said mutation or combination of mutations by a resistance coefficient  $\beta_A, \beta_B, \dots, \beta_Z$ ;

wherein for a combination of mutations, said the mutation factor  $M_n$  represents the co-occurrence of one mutation with other one or more mutations and said the coefficient  $\beta_n$  represents the synergy or antagonism between said the one mutation with said the other one or more mutations;

wherein said the mutation factor assigned to each said mutation or combination of mutations reflects the degree to which said mutation or combination of mutations is present in said HIV strain and, if present, to which degree said the mutation is present in a mixture;

wherein each said resistance coefficient reflects the contribution of said the mutation or combination of mutations to said the fold resistance exhibited by said strain;

wherein the error term  $\varepsilon$ , represents the difference between a modeled modelled prediction and an experimentally determined measurement;

2) replacing wherein the censored values in said data from said dataset of matching genotype and phenotype database are replaced by a maximum likelihood estimation;

wherein for each iteration of said linear regression, said maximum likelihood estimation is generated according to the following steps:

wherein for each iteration of the linear regression, the following steps are performed until the predictions converge:

a) calculating a linear regression model without said censored values;

b) using a phenotypic measured value  $V_0$  of said data of said dataset of matching genotypes and phenotypes as if the censor was “=”, when a result is expressed as  $-\log FR < 4$ ,  $V_0$  is treated as  $-\log FR = 4$ ;

c) using looking at the prediction P from the said linear regression model to and apply either:

When said phenotypic value is smaller than said range, ease a ‘<’-censor is applied to said value:

i)  $P < V_0 - 0.798 \sigma$  (center of gravity of half Gaussian distribution)

Remove value from training data for the next iteration

ii)  $V_0 - 0.798 \sigma \leq P < V_0$

Use  $V' = V_0 - 0.798 \sigma$  for the next iteration

iii)  $V_0 \leq P$

Use  $V'$  center centre of gravity of tail ( $<V$ ) of a normal distribution  $N(P, \sigma)$  as value for the next iteration

When said phenotypic value is higher than said range, ease a ‘>’-censor is applied to said value:

i)  $P > V_0 + 0.798 \sigma$  (center of gravity of half Gaussian distribution)

Remove value from training data for the next iteration

ii)  $V_0 + 0.798 \sigma \geq P > V_0$

Use  $V' = V_0 - 0.798 \sigma$  for the next iteration

iii)  $V_0 \geq P$

Use  $V'$  center centre of gravity of tail ( $>V$ ) of a normal distribution  $N(P, \sigma)$  as value for the next iteration;

- d) calculating a linear regression model and for said the censored values in said the linear regression model, either remove the data-point from the training set, or use  $V'$  instead of the censored phenotypes measurement, as described in step c);
- e) reiterating from steps b) to d) until the prediction converges; thereby quantitating the individual contribution of said mutation or combination of mutations to said a drug resistance phenotype exhibited by said HIV strain.

7. to 16. (Canceled).